

# 5

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## RAW SEQUENCE LISTING

DATE: 12/07/2001

PATENT APPLICATION: US/09/932,888

TIME: 16:40:05

Input Set : N:\Crf3\RULE60\09932888.txt

Output Set: N:\CRF3\12072001\I932888.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: Bidwell, Christopher A.  
7 Spurlock, Michael E.  
9 (ii) TITLE OF INVENTION: PORCINE LEPTIN PROTEIN, NUCLEIC ACID  
10 SEQUENCES CODING THEREFOR AND USES THEREOF  
12 (iii) NUMBER OF SEQUENCES: 8  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.  
16 (B) STREET: Suite 2100 111 East Wisconsin Avenue  
17 (C) CITY: Milwaukee  
18 (D) STATE: Wisconsin  
19 (E) COUNTRY: USA  
20 (F) ZIP: 53202  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Floppy disk  
24 (B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
28 (vi) CURRENT APPLICATION DATA:  
C--> 29 (A) APPLICATION NUMBER: US/09/932,888  
C--> 30 (B) FILING DATE: 07-Jun-2001  
31 (C) CLASSIFICATION:  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: US 08/692,922  
35 (B) FILING DATE: 31-JUL-1996  
39 (viii) ATTORNEY/AGENT INFORMATION:  
40 (A) NAME: Shaw, Melissa A.  
41 (B) REGISTRATION NUMBER: 38,301  
42 (C) REFERENCE/DOCKET NUMBER: PM-8935  
44 (ix) TELECOMMUNICATION INFORMATION:  
45 (A) TELEPHONE: 414-273-2100  
46 (B) TELEFAX: 414-223-5000  
49 (2) INFORMATION FOR SEQ ID NO: 1:  
51 (i) SEQUENCE CHARACTERISTICS:  
52 (A) LENGTH: 5917 base pairs  
53 (B) TYPE: nucleic acid  
54 (C) STRANDEDNESS: single  
55 (D) TOPOLOGY: linear  
57 (ii) MOLECULE TYPE: DNA (genomic)  
60 (ix) FEATURE:  
61 (A) NAME/KEY: CDS  
62 (B) LOCATION: join(942..1085, 3400..3753)  
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
67 AAGCTTTCTT GGCCCTAAC AGCAACCACA TTATACTCTT ACTGGCTATT CCTTGGCCTT 60  
69 CAATACCCAG CCCAGGGGAC CCCTCTTCCA GGGAGCCCCG CTTGTACTCC TGAGATGTCA 120  
71 TGTCTTCTT GCAGAGCTCT TCCTCACGGC ATCGGGACGG CGGTTACCC TTTTGCCTCT 180

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73	CCGGATAAAC	TGTAAGCTAC	TTGAGAGCAG	AGAACATCCA	TTGTTGCTG	TGGCATCCGT	240
75	GGTACCTAGC	ACGGCATCTG	ACATATTATC	AGATCTTCCA	CAAAGGCCAG	TTTACGGTTG	300
77	AATGCCCCGT	GAATTCAGGC	TCCCAGTGGG	AGAGCGAGGA	AGTAATAAAG	CCGGTGATAA	360
79	ATGCCGCCGT	GGAGACACCA	GCGGGCTGCC	GTGAGACTAA	TGGAGAGGAC	AGTAACGTTA	420
81	TCTCTAATGC	GAGGGTGGTT	ATAGAGTACA	TTTCATAACA	CCTTTAAAGC	TCTTTCACAC	480
83	GCATTATCCA	ATTTGATCCT	CATAAAAGCC	TGGAGATGTG	TATATTGTGG	TGGATGGAGG	540
85	GGGAGTCTTT	AGCAGTTATG	GGATATGCCT	GAAGTCGTGC	AGCTAGTAAA	TGGCTGGATT	600
87	CAAACCAGAC	CTCAAAAGCC	TGCCTGTTTG	CTCATGCCCC	CTGCCCCGAC	TGCCCCACTCT	660
89	GTGGCCACAC	GCACAACTCA	CCGTGCGCTTT	CTTGATCCGT	TTTCTTGATC	CGGCTGTGCT	720
91	CTCCCCAAGG	AATGCTTTTC	ATTAACATAT	GTCTAGGTAA	TGAATTATCT	TGACTCTGAG	780
93	GAGGCCATAG	CACATGCCGT	AACGCGACAG	CTCCTTTGAT	CTGCATCTGA	GGCTGTGGCT	840
95	GGTAACGGGC	GTGGGGAGGG	GGCGTTGCT	GAGACCCAG	GGACACGCCA	TGTGTGGTTC	900
97	CCTCTGTTTC	CAGGCCCCAG	AAGCACATCC	CGGAAAGGAA	A ATG CGC TGT GGA		953
98					Met Arg Cys Gly		
99					1		
101	CCC CTG TGC CGA TTC CTG CTG GCT TTG GCC TAT CTG TCC TAC GTT GAA						1001
102	Pro Leu Cys Arg Phe Leu Leu Ala Leu Ala Tyr Leu Ser Tyr Val Glu						
103	5 10 15 20						
105	GCC GTG CCC ATC TGG AGA GTC CAG GAT GAC ACC AAA ACC CTC ATC AAG						1049
106	Ala Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys Thr Leu Ile Lys						
107	25 30 35						
109	ACG ATT GTC ACC AGG ATC AGT GAC ATT TCA CAC ATG GTAGGGAAGG						1095
110	Thr Ile Val Thr Arg Ile Ser Asp Ile Ser His Met						
111	40 45						
113	CCTGGGAGAC AAGGTGCAAC CTGTGGCCAG CCCSGGGGGA GGAGGGGTAC CGGACCTCAG						1155
115	AGGTTGGCGG AGGTGGGAAG GGTCGGCGGT GGCCTTGACG CCTCCCCCAC CCCCCCAAC						1215
117	CAGCTGCCTT TGCTCCTCCG CTTCCCTCAC CGCACCCCC CACGTCCTTA TCCTCCTTCT						1275
119	TCCCAGACTG GAATCCTGAT GCCCAGGACT AGAGGAAGCC CTAAAGGTCC TGTGTGCCTT						1335
121	TGCCAGGTGC GCAGACCCCC CAGCATCATC CCCTCTGGCC TCCATCACGT CTCCGGAATG						1395
123	TTCTAATCTG TAGGAATTCT TCCTGGTGAC AGCTGAACTC TGACCCTGCG GACGCCCTT						1455
125	ACTGCTAGTC CTGCCCATTG AGCCTTTTTT CCTATACAAC CCTCTACATG TTTGCAAAC						1515
127	TCTCTCAATG TCCCCAGGGT GTTTTCTCTG GGGTCCGAG GCCGAGACCT TCAGCCTCTT						1575
129	CTCAGCTGAG GTCCGTCTTT AGAATTGAGA AGACAGGGTG TGACTCCTCA CCCTGTGTT						1635
131	CCCTCTCTGT AAAATCTCAA GCACGTTAAG TCCCTCCGTG TCTGAAACCT TAGTTTCCCT						1695
133	CATCCAGATA ATGGGACTGT TACTGGGAAG ATGTTACCGG AATCCAGGGT CTTGCCTCAT						1755
135	GGAGCTCAAG AATGAACTTG GCGAACGCAC AGGGAGCCGA GCAAGCAGAA GTCTTTATTA						1815
137	CAGGAAGGCA GACAGCTCCC AGCACAGACA CGGGGAGGGA AGAGTCCCC CGCCCATTGT						1875
139	TCTACGGAGG TTTTATCAC TTAAAGACGG GAGTACCAAT GTGGGGTCCA GATATCCGTT						1935
141	CTTCTTCCCA TTGCCAGTT TACCTATATG GCGCCTTGTC CAGGAGGGAC TCTGTAGAGT						1995
143	TAGGGGTGCT CCGTAAGTTT TATGGTGCCT CTGCTCTTCT CTGCCCTAGA CTTAGAGTCG						2055
145	CCACTCTTTC CATTCTTCTG CTCACAGTCA AATGCATAGG TCAGGGGTTA ATTCCACCT						2115
147	TCACAGAAAT CAAATGTCCT TTCAATAGTT AATCTTCCAA TAAGCAAGGC CTGCTTGCT						2175
149	TGATTAGTTT TTACAAATCT TAAACCATGG CCATTAATCA GGGAAGAGAT CGAAGCCCAT						2235
151	GTTCCACAC TAAGTGCCTG AATTATTAGT CTGCCTCAGG ACTATCTTAA TAGTCTTCGC						2295
153	AAGGTTGTTT TGAGATTAAA TTAGATAGGA GTTCCTGTG AGGCGCGACG GAAACAGATC						2355
155	CGACTCAGAA CCATGAGACA GGTTCGATCC CTGGCTTTGT CAGTGGGTTA GGATCTGGTG						2415
157	CTGCTGTGAG CTGTGGTGTA GGTGCGAGAG GTGGCTCGGA TCCCGCGTTG CTGTGGCTGT						2475
159	GGTGTAGGCC GGTGCAGACA GCTCCGATTA GACCCCTAGC CTGGGAACCT CCATGTGCCG						2535
161	CGGGTACCGC TAAAAAAGA CAAAAGATGG AAAAAAATAA GGTTACATTA GATAAAGCAA						2595

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163	GTGACTCCTC	CACCACCACA	CATATCCCTG	CAGAACCAGG	ACAGAGCATG	CCTTCTTGAA	2655
165	AAGTTTTCGG	TTGTGGCTTT	GATAGCACCC	AGCCTTAAAA	GCCAGCTTTT	CAATCTGCCC	2715
167	AGAGCAGTCT	GGAGACTTCC	GCATCTCCTG	GCCACTCTGA	GTTTCTAACA	GTGGCCTTGG	2775
169	CGAGCCTGGG	AGCAGTCCGG	TGGCCAGAAG	CAGGGACAGC	TGAGAACCAG	ATAGAGTCTT	2835
171	GGCACTTTCA	AGAGAAAACC	CTAAGTCTCC	TTCTTCCAGC	CATGCAACAG	CTGCGCATGA	2895
173	CAGATCCAGC	GTGTCCCAGC	CTGTGTGGTG	CAGGGAGTGA	YGCTGCGNNY	AGGGYGYGGG	2955
175	GGAGCTGAGG	AGCGAGGCGG	GGCATCGNGG	GGCTGCAGCC	TCCATCCCTA	AGTGGGGAGA	3015
177	CTTCATGAAG	AGCCTGACCA	GNAGGGAGGG	GCATGTGTGG	AGGACCTCAG	GGCCTGGGGA	3075
179	AGGCTAGACC	CAACTATGTG	AGAAACAGAC	AGTCGTGGCT	GGTTCTACAG	AAGAGGCATC	3135
181	TGGAGGCCAT	TCGAATGCCC	AAAGCTGTCT	GGGTGAGGCA	GGGCTTGCTA	GGCAGAAGAC	3195
183	AGAAGGCCGT	GAGACCAGCT	TGGAGGCTTG	GCAGCCACGC	CAGCCCAAGG	AGTTCGGGCC	3255
185	TAGATAGGAT	TGTGTGGAAG	GGGAAGAGGC	AGCCGGAGGT	GGGGGGTGGG	GGTGGACCCG	3315
187	TCTCCACGCC	TGCAGGAAGG	CCAGGGGCTG	CAGAGCCAAC	ATCTCTCTCG	CTGAGCGTCT	3375
189	CGCTCTCCCC	TTCTCTCTGC	ACAG CAG TCT GTC TCC TCC AAA CAG AGG GTC				3426
190			Gln Ser Val Ser Ser Lys Gln Arg Val				
191			50		55		
193	ACC GGT TTG GAC TTC ATC CCT GGG CTC CAT CCT GTC CTG AGT TTG TCC						3474
194	Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Val Leu Ser Leu Ser						
195	60		65		70		
197	AAG ATG GAC CAG ACC CTG GCG ATC TAC CAA CAG ATC CTC ACC AGT CTG						3522
198	Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile Leu Thr Ser Leu						
199	75		80		85		
201	CCT TCC AGA AAT GTG ATC CAA ATA TCG AAT GAC CTG GAG AAC CTC CGG						3570
202	Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg						
203	90		95		100		105
205	GAC CTT CTC CAC CTG CTG GCC TCC TCC AAG AGC TGC CCC TTG CCC AGC						3618
206	Asp Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys Pro Leu Pro Ser						
207	110		115		120		
209	AGG GCC CTG GAG ACC TTG GAG AGC CTG GGC GGC GTC CTG GAA GCC TCC						3666
210	Arg Ala Leu Glu Thr Leu Glu Ser Leu Gly Gly Val Leu Glu Ala Ser						
211	125		130		135		
213	CTC TAC TCC ACG GAG GTG GTG GCC CTG AGC AGG CTG CAG GGG GCT CTG						3714
214	Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ala Leu						
215	140		145		150		
217	CAG GAC ATG CTG CGG CAG CTG GAC CTC AGC CCT GGC TGC TGAAGCCTTG						3763
218	Gln Asp Met Leu Arg Gln Leu Asp Leu Ser Pro Gly Cys						
219	155		160		165		
221	AAGGCCTCTC	TCCCCACAGT	CGGGGGAAGA	AACCTGAGCT	TCCAGGAGTC	TGCTGGAGAA	3823
223	GAGAGCCTGT	GCGGACCTCC	TCTCTGCAGG	TCTGCGGACC	ATTTCTCTCT	CGCTCCGCTA	3883
225	AGCTGCTCTT	CCAAAGGCAG	AAAACCTCAA	GGCACGACAC	CAAAGACAGA	AAGGCCTGGT	3943
227	TCCGCGCCCA	CCGAAAGGG	GGCGCCGTCC	AGCCAACGGT	GGACTAGATT	TCGGATTTTC	4003
229	CACCAACGTC	TTCTTCCCTG	TTCCATCTCC	AGCTCACCGC	GTGCTTCAGC	GTGACCGGGG	4063
231	GGATTTTCAGA	GCCTTTCGAC	CATCAAGCAG	GGTTCCATCT	GAGAATTCCG	GGGAGCACGG	4123
233	TGAAGGCTAC	AGGCACACAC	AGCTGGATGC	TCCCACGCAA	CACAAGTTGG	AAGCATTTCT	4183
235	TTATTTATTA	TGCGGTGTAT	TCTGGTTGGA	TTTGAAGCAA	AACACCAGCC	TTTCCAGGCT	4243
237	CTCTGGGGTC	AGCCGGGGCT	AGGGGGAGGC	TCCCGAGGTG	CTGTTTCCAG	TACCATCCAT	4303
239	GGGCCTGCTG	AGGCCAACCC	ATTTTGAGTG	ACTTGAGGGC	TCTCAAGGTC	GTTCTCTAGA	4363
241	GACTGGCTTT	GTTTCTACTG	TGACTGACTT	TAAAACTGCA	GCGTGTGCAC	TGGCATCGCC	4423
243	TGCGCGGATC	TCGAAGGGCC	AGGTTCTCTT	AGAAAGAAGA	AGATGAACTT	TGTCAGGGGT	4483

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245 GTGTACGCGG AGACAGGAAG TGTGTTGGTG GCGGGGCGAT GGATCCAGAA TGTGTATTTT 4543
247 TTGTGTGATG GACATTTGTG TGAGGGGCTC TCTGGACAGG GTGAGGTCAT TGTCTCATCT 4603
249 TCGTGGTTTT CATGAGAGAA GGAGATGATT CCTTCACGGG GGTCGTGGGG TTTTGCCAGC 4663
251 CGCCCGTGCA GGAGTGGGGA AGGGGCTGAA GCCGAAGACC GTTGGGGGCC GTGGTGAGCT 4723
253 CTGCCTTCTC CAGCTGCTAG AGGCTGGTCT TTCTCATCAG GGAGTGAGGG TCTCGCGTTG 4783
255 GAGACAGTGA TCCCCAGGGC GGGATCCTTG CCGTGGCCCT CTGAATGGTC TGGGTGATCC 4843
257 CACACTGATG TCATAACAGG GAAGTGCCTT GGTTCGGGAT TTGTATGCTC ACCCAAAGCA 4903
259 AGGGCCTGCT TCCCATCCAT TTTGGGAAGG ATTTTTTCTC CAGGGGGAGG GTGAAAGCTC 4963
261 TGGGAGGTCT GTGGGCTTAC GAGATGGTCC AAGTCCTGGG TCAGTGAGTC CCGGGACTCG 5023
263 TGACCGCCTC GAGGAGCCCC CTTCTCCCTA CAGGTCATGT TCAATAGGTC AAACAAGGAG 5083
265 GCATGGGTTT CCACCATCCT GCCGCTGTGA TGCAGCCATC GCACTACAGG AGGTAGATCT 5143
267 GTCCAAGGAA ATTTGAATCT CAAGCAATCA CTTTCAAGAC TGAGCATCTA TTGTGCTCAG 5203
269 CCCCAACTGG TGCTATGGGC TCAGAGAAGC TCATCAAATA AATATTAAAA TCCAGTCCTG 5263
271 CCTTCAGGAC CTTGCATTCC AGATGATAAC ACCTCCCCCA CACCCCGTCT GCAGAGGCTG 5323
273 TCATTTCAAC ATGGCAACCG AGCAGCTGAA ACACAGTGCG GTCCTCAGCA GGTGGAAAGG 5383
275 CTGAGCTGAG GAGGGCAGTG CCCGGGCCCC CAGGCTAACC CTGCTTGAC TTGGTAGCAT 5443
277 TTTTACTGTT CGGGGCGCAT CAGCATCTAT TACTGAGAAG CCGCATCCCT TTGAAGCAGG 5503
279 ATAGCTGAGA CTATAAAAAA AAGAAAATAC CAGAGTTCCC TTGTGGCACA GAGGGCTAAG 5563
281 GATCCAGTGT TGTGCTGCA GCAGCTTGGG TCACGGCTGT GGCAAGGGTT CGATCCCTGG 5623
283 CCTGGGAACT TTCACATGTT GCAGGCAAGG CCAAAAAAAA ATAAATAAAT AAAAATAAAC 5683
285 AAAAAAAAAC AAGACCATAA CAGCAGACTG GTGGCAAACC AGGACTAGAA CCTGGGTCCT 5743
287 CTGACCCCTA GAGTCAGTGT CCCCTGAGCC AGCTAGTGTT CTCTGGGGAC GGGAACAGGG 5803
289 TTGGGCAGGG AGTTCAGGAA GTGTTTGCTG GAAGAGCGGA GTTTCAGGC TGATTTTGCA 5863
291 GGAGGTGAGG GAAGTGGATT GCCTGGAGGG AGGAGGCTGT TTTGTTTGAA GCTT 5917

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294 (2) INFORMATION FOR SEQ ID NO: 2:

296 (i) SEQUENCE CHARACTERISTICS:

297 (A) LENGTH: 166 amino acids

298 (B) TYPE: amino acid

299 (D) TOPOLOGY: linear

301 (ii) MOLECULE TYPE: protein

303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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305 Met Arg Cys Gly Pro Leu Cys Arg Phe Leu Leu Ala Leu Ala Tyr Leu
306 1 5 10 15
308 Ser Tyr Val Glu Ala Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys
309 20 25 30
311 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Ser Asp Ile Ser His Met
312 35 40 45
314 Gln Ser Val Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
315 50 55 60
317 Gly Leu His Pro Val Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
318 65 70 75 80
320 Ile Tyr Gln Gln Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Ile Gln
321 85 90 95
323 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
324 100 105 110
326 Ser Ser Lys Ser Cys Pro Leu Pro Ser Arg Ala Leu Glu Thr Leu Glu
327 115 120 125
329 Ser Leu Gly Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
330 130 135 140

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332 Ala Leu Ser Arg Leu Gln Gly Ala Leu Gln Asp Met Leu Arg Gln Leu
333 145                      150                      155                      160
335 Asp Leu Ser Pro Gly Cys
336                      165
338 (2) INFORMATION FOR SEQ ID NO: 3:
340   (i) SEQUENCE CHARACTERISTICS:
341       (A) LENGTH: 435 base pairs
342       (B) TYPE: nucleic acid
343       (C) STRANDEDNESS: single
344       (D) TOPOLOGY: linear
346   (ii) MOLECULE TYPE: cDNA
349   (ix) FEATURE:
350       (A) NAME/KEY: CDS
351       (B) LOCATION: 1..435
354   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
356 GTG CCC ATC TGG AGA GTC CAG GAT GAC ACC AAA ACC CTC ATC AAG ACG      48
357 Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
358 1      5      10      15
360 ATT GTC ACC AGG ATC AGT GAC ATT TCA CAC ATG CAG TCT GTC TCC TCC      96
361 Ile Val Thr Arg Ile Ser Asp Ile Ser His Met Gln Ser Val Ser Ser
362      20      25      30
364 AAA CAG AGG GTC ACC GGT TTG GAC TTC ATC CCT GGG CTC CAT CCT GTC      144
365 Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Val
366      35      40      45
368 CTG AGT TTG TCC AAG ATG GAC CAG ACC CTG GCG ATC TAC CAA CAG ATC      192
369 Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile
370      50      55      60
372 CTC ACC AGT CTG CCT TCC AGA AAT GTG ATC CAA ATA TCG AAT GAC CTG      240
373 Leu Thr Ser Leu Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu
374 65      70      75      80
376 GAG AAC CTC CGG GAC CTT CTC CAC CTG CTG GCC TCC TCC AAG AGC TGC      288
377 Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys
378      85      90      95
380 CCC TTG CCC AGC AGG GCC CTG GAG ACC TTG GAG AGC CTG GGC GGC GTC      336
381 Pro Leu Pro Ser Arg Ala Leu Glu Thr Leu Glu Ser Leu Gly Gly Val
382      100      105      110
384 CTG GAA GCC TCC CTC TAC TCC ACG GAG GTG GTG GCC CTG AGC AGG CTG      384
385 Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu
386      115      120      125
388 CAG GGG GCT CTG CAG GAC ATG CTG CGG CAC GTG GAC CTC AGC CCT GGC      432
389 Gln Gly Ala Leu Gln Asp Met Leu Arg His Val Asp Leu Ser Pro Gly
390      130      135      140
392 TGC      435
393 Cys
394 145
397 (2) INFORMATION FOR SEQ ID NO: 4:
399   (i) SEQUENCE CHARACTERISTICS:
400       (A) LENGTH: 145 amino acids
401       (B) TYPE: amino acid

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09932888.txt

Output Set: N:\CRF3\12072001\I932888.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]